

651 CATTTCCTTGGGCTTTGGCTTTATGCTTCCTCCTCATGGCTTAAGT 700

```
seq_name. /Slit2/seqdata/geneseq/NA2000.DAT:AAA95105
seq_documentation_block:
ID AAA95105 standard; DNA; 1368 BP.
XX
XX AAA95105;
XX
XX 12-JAN-2001 (first entry)
XX
XX human TNFR1 coding sequence.
XX
XX
XX TNFR1; tumour necrosis factor receptor; polymorphism, human;
XX tumour; cancer; apoptosis; bacterial infection; ds.
XX
XX homo sapiens.
XX
XX
```



```

34 euGlyAspArgGlyLysArgAspSerValCysProGlnGlyLysTyrIle 50
1187 TCGGACAGAGGAGAGAGACAGACATAGTGTGTCGCCCAAGGAAAATATATC 336
51 HisProGlnAsnAsuSerIleCysCysThrLysCysHisLysGlyThrTy 67
1237 CTAGACATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1486
367 proLeuArgTrpIleLysGluPheValArgLeuGlyLeuSerAspHisG 384
1287 CCGGTCGCGGTCGAAAGAAATTCGGTGGCGGCGGCTAGCGGCTGAGCGACCC 1336
384 LuLeuAspArgLeuGlnLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
1337 AGATCATCGCGTGGAGCTGGAGAACGGGGCTGGCTGGCGGGAGGGGCAA 1386
401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417
1387 TACAGCATGCTGTGATGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1436
417 PheGluLeuLeuGlyArgValLeuArgAspMetAspLeuGlyCysL 434
1437 GCTGAGCTGTGGGACCGCGTCTCGCGGCAATGAGCTGTGGCTGGC 1486
434 euGluAspIleGluAlaLeuGlyGlyProAlaAlaLeuProProAla 450
1487 TGGAGGACATTCAGGAGCGGCTTTCGGGCGCGCGCGCGCGCGCGCGG 1536
451 ProSerLeuLeuArg 455
1537 CCGAGCTCTCTCGAGA 1551

seq_name: /SIN523cdata/4cncseq/4cncseq/NA2000.LAT.AA.48475
seq_documentation_block:
ID AA248475 standard; DNA: 2161 BP.
XX
XX AA248475;
XX
XX 31-MAR-2000 (first entry)
XX
DE Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
XX inflammation; tumour formation; TNFR1; anticancer; ds.
XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PP 26-JUN-1998; 98US-0106038.
XX
PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM INC.
PI Baker HF, Cowdell LM;
XX
DR WPI: 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
XX diagnosis, treatment and prevention of disease, particularly tumors
XX
XX Example 10; Columns 33-36; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
XX necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
XX can be used in a method of inhibiting the expression of TNFR1 human cells
XX or tissues. The antisense compounds specifically hybridize with one or
XX more nucleic acids encoding TNFR1 modulating the function of nucleic
XX acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1

```

```

34 euGlyAspArgGlyLysArgAspSerValCysProGlnGlyLysTyrIle 50
287 TAGGACAGAGGAGAGAGACAGACATAGTGTGTCGCCCAAGGAAAATATATC 336
51 HisProGlnAsnAsuSerIleCysCysThrLysCysHisLysGlyThrTy 67
337 CAGGCTCAAAATATTCGATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAG 386
67 PheGluLeuLeuGlyArgValLeuArgAspMetAspLeuGlyCysL 84
387 CTGTGATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 436
84 YsgLysSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
437 GTGACAGCGGCTGCTTCCACCGCTCAGAAAACCCAGCTCAGACACAGCTC 486
101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117
487 AGCTGCTCCAAATGCGGAAAGGAAATGGCTAGCTGAGAGATCTCTCTTG 536
117 SThrValAspArgAspThrValCysGlyCysArgLysAsnGlnIleArgH 134
537 CACAGTGTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 586
134 IstYrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
587 ATTATGGAGACGAAACCTTTCACACTGCTTCAAATTCAGAGCTCTGCTC 636
151 AsnGlyThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 167
637 AATGAGAGAGTGTGATCTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 686
167 PysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
687 CTATATATATATATATATATATATATATATATATATATATATATATAT 736
184 snCysLysLysSerLeuGlnGlyThrLysLeuCysLeuProGlnIleGlu 200
737 ACCTGTAAGAAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217
787 AATGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 836
217 IstPhePheGlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetT 234
837 CATTTCTTTGGCTTTGGCTTTTATGCTTCTCTTCAATGGTTTAATGT 886
234 YrArgTyrlaArgTrpLysSerLysLeuTyrSerIleValCysGlyLys 250
887 ATGGCTTACCAACGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
251 SerThrProGlyLysGlnGlyGlnGlnGlnGlnGlnGlnGlnGlnGln 267
937 TGACACCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
267 uAlaProAsnProSerPheSerProGlnProGlyPheThrProThrLeuG 284
987 GGGCGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1036
284 LysPheSerProValProSerSerThrPheThrSerSerSerThrThrTh 300
1037 GCTTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317
1087 CCGAGTGTATGTCTCAATTTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1136
317 GlyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaGArgAspProI 334
1137 CTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1186

```



```

OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 256..1673
FT /*tag= a
FT /product= p55 TNF-R
FT misc_signal 2143..2149
FT /*tag= b
FT /note= "possible poly-A signal"
FI
FX
PN A09475742-A.
XX
XX 04-MAY-1995.
XX
XX 11-OCT-1994; 94AU-0075742.
XX
XX 12-OCT-1993; 9311-0107268.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
PA
PI Ratkin M, Brakebusch C, Varfolomeev B, Wallach D;
DR WPI: 1995-194342/26.
DR P PSDB: AAR750R4.
XX
XX New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF receptor, useful for
PT antagonising deleterious effects of TNF.
PS
PS Disclosure: Fig 1. 40pp. English.
XX
XX This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
XX Expression of this receptor is regulated by shedding of the
XX extracellular receptor fragment. The p55 TNF-R can be shed in response
XX to different inducing agents, e.g. phorbol myristate acetate (PMA),
XX depending on cell type. The only region of the receptor whose structure
XX affects the shedding response is the spacer region (see AAR75012) in the
XX extracellular domain. This region is located close to a site of cleavage
XX of the molecule, and links the cysteine-rich module to the transmembrane
XX domain. The spacer region of the cloned p55 TNF-R was used to create the
XX chimeras between human p55 TNF-R and murine epidermal growth factor
XX receptor (EGF-R) that are represented by AAR75007-11. This spacer region
XX was subjected to deletion mutations (AAR75013-25) and substitutions
XX (AAR75026-47) of the spacer region. The most important residues are
XX Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
XX important of these. The shedding of the receptor is independent of the
XX side chain identity of these residues, with the exception of a limited
XX dependence on the identity of Val 173. Mutations which alter the
XX conformation of the protein adversely effect the shedding process. The
XX mutations shown in AAR75013-47 were introduced in order to create an
XX inhibitor of a protease that is capable of cleaving the soluble TNF-R
XX from the cell bound TNF-R. Fragments of these inhibitors can be seen in
XX AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
XX inhibitors can be used for enhancing TNF function.
XX
XX Sequence 2175 RP: 474 A: 642 C: 603 G: 456 T: 0 other:

```

```

alignment_scores:
  Quality: 2487.00      Length: 455
  Ratio: 5.466         Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
us-09-525-998a-2 x AAQ90513
Align seq 1/1 to: AAQ90513 from: 1 to: 2175
1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuLeuG 17
|||||
256 AAGGAGCTCTCCAGGATGCGGACCTGCTGGCGGCGGCTGCTCGA 305
17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34
|||||
306 GCTGTTGCTGGCAATATATACCTCAGGGGTTATTGGACTGAGCTCACC 355
34 euGlyAspArgGlyLysArgAspSerValCysProGlnGlyLysTyrIle 50
|||||
355 TATGGAAATAGGAAATAGATATGTTGTGTCCCAAGGAAAAATATATC 405
51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67
|||||
406 CACCCCTCAAAATAATTCGATTTCCTGACCAAGTCCCAAGGAAGGACIA 455
67 rLeuTyrAsnAspCysProGlyGlnAspThrAspCysArgGluC 84
|||||
456 ATTGTATATATATATATATATATATATATATATATATATATATATAT 505
84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
|||||
506 CTGAGAAAGGATCTTCTTATATATATATATATATATATATATATATAT 555
101 SerCysSerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCy 117
|||||
556 ACTGTCTTCTCAATGCTGAAAGAAATGGGTGAGGTGGAGATCTCTCTTG 605
117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
|||||
606 CATATAGAGAAAGGATCTTCTTATATATATATATATATATATATATAT 655
134 isTyrTrpSerGluAsnLeuPheGlnCysPheAspCysSerLeuCysLeu 150
|||||
656 ATTATAGAGAAAGGATCTTCTTATATATATATATATATATATATATAT 705
151 AsnGlyThrValHisLeuSerCysGlnGlyLysGlnAsnThrValCysTh 167
|||||
706 AATGGGACCGTCTGACCTCTCTGCTCAGGAGAAATAGAACACCGTGTGC 755
167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
|||||
756 CTGTATATATATATATATATATATATATATATATATATATATATATAT 805
184 sGlyCysGlySerLeuLeuGlyCysThrLysLeuCysLeuGlnLeuLeu 200
|||||
806 ATGTATATATATATATATATATATATATATATATATATATATATATAT 855
201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217
|||||
856 AATGTTAAGGGGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 905
217 HisPhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMet 234
|||||
906 CATTTCTTTTGGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCT 955
234 TTAATGTTCTTAATGTTCTTAATGTTCTTAATGTTCTTAATGTTCTTAAT 955
955 ATATGTTCTTAATGTTCTTAATGTTCTTAATGTTCTTAATGTTCTTAAT 1005
251 SerThrProGluLysGlyGlyLeuGlyGlyThrThrThrLysProLe 267
|||||
1006 TGTGACACCTGAAAAAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1055
267 uAlaProAspProSerPheSerProThrProGlyPheThrProThrLeuG 284
|||||
1056 GATATATATATATATATATATATATATATATATATATATATATATAT 1105
284 LysSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
|||||
1106 GATTCAGTCCGTTGCGGAGATTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1155
301 ProGlyAspCysProAspPheAlaProArgArgGlnValAlaProPr 317
|||||
1156 CCGGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
317 tTyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspPro 334
|||||

```



```

356 TAGGGACACGGACACACAGATAGTAGTGTGTGTGTCGACAGGAAAAATATATC 405
51 HisProGlnAsnAsnSerIleCysCysThrIysCysHisIysCysIleThr 67
1406 CACCCCTCAAAATATTCGATTCCTGTACCAAGTGCACAAAGGAACCTCA 455
67 IleuIyrAsnAspCysProGlyGlnAspThrAspCysAspGluC 84
1456 CTGTGTAATGACCTGCTGACAGGACAGGACAGGACAGGACAGGACAGG 505
84 YSGLuSerGlySerPheThrAlaSerGluAsnHisIeuArgHisCysIeu 100
1406 GTGAGAGGGCTCTCTTACCTGCTTACAGAAACACCTCAGACAGGCTC 555
103 SerCysSerIysCysAspGlySerIleCysCysIleValIleIleSerSerCys 117
556 AGCTGCTCCAAATGCTGAAAGGAAATGCGTTCAGGTGAGTATCTCTTC 605
117 sThrValAspAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
606 CACAGTGGACCGGACACCGTGTGCTGCTGCGAGGAGAAACCACTACCG 555
134 IAspIyrSerGluAsnIleuPheGlyCysIleAspCysSerIeuCysIeu 150
656 ATTATTGAGAGGAAACCTTTTCAATGCTTCAATGAGAGCTCTGCGCTC 705
151 AsnGlyThrValHisIeuSerCysGlnGluIysGlnAsnThrValCysThr 167
706 AATGGACCGTGCACCTCTCCCTGCGAGGAGAAACAAACACCGTGTG 755
167 rCysHisAlaGlyPhePheLeuArgLysAsnGluCysValSerCysSerA 184
756 CTGCAATGCAAGGTTCTTCTTAAAGAAACCACTGCTGCTGCTGCTG 805
184 sNcysIysIysSerIeuIleuIysThrIysCysIleuIleuIleuIleu 200
806 ACTGTAGAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
201 AsnValIysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217
856 AATGTTAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
217 IlePhePheGlyLeuIysLeuSerLeuLeuPheIleGlyLeuMetI 234
906 CATTTCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 955
234 YrArgIyrGlnArgIyrSerIysLeuIyrSerIleValCysGlyIys 250
956 ATGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
251 SerIthrProGluIysGluGlyGluIleuGlyGlyThrThrThrIysProLeu 267
1006 TGCACAGCTGAAAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1055
267 uAlaProAsnProSerPheSerProThrProThrPheThrProThrLeuG 284
1056 GGGGCCCCAAACCCCAAGCTTACAGTATACAGAGCTTCAAGGAGGAGG 1105
284 IyheSerProValProSerSerIthrPheThrSerSerIthrIyrThr 300
1106 GTTCAGTGGGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 1155
301 ProGlyAspCysProAsnIleAlaProArgArgGluValAlaIleProI 317
1156 CCGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205
317 cTyGlnGlyValAspProIleLeuAlaThrAlaLeuAlaSerAspProI 334
1206 CTAICAGGAGGCTGAGTCCCAATCTTCCGAGAGGAGGAGGAGGAGGAG 1255
334 IeProAsnProLeuGlnIysIyrGluAspSerAlaHisIysProGlnSer 350
1256 TGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305

```

```

351 LeuAspThrAspAspProAlaThrIeuTyrAlaValValIleAsnValPr 467
1306 CTACACACACACACACACACACACACACACACACACACACACACAC 1455
367 GProLeuAspIlePylAspIleValIleArgIleGlyIleGlyIleGly 484
1456 CCGATTTGGATTCAGAGGAAATGGTGTGGAGGCTAGAGAGATGAGAG 1405
384 ILeuAspAlaIleuGlnIleuGlnAspIleuArgCysIleuArgIleuAla 400
1406 AGATTCATACAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1455
401 TyrSerMetIeuAlaThrIrpArgArgThrProArgArgArgIleuAla 417
1456 TATAGCATGCTGGCGAGCTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1505
417 rLeuGluLeuLeuGlyArgValIleuArgAspMetAspLeuLeuGlyCysL 434
1506 GTGGAGCTGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1555
434 euGluAspIleGluGlnAlaIleuCysGlyProAlaAlaIleuIleuProAla 450
1556 IeAspAspAlaIleuAspAspIleuGlnGlnGlnGlnGlnGlnGln 1605
451 ProSerLeuIleuArg 455
1606 CCGAGCTGTGCTGCA 1620

seq_name: us-09-525-998a-2.rng; Pos: 100; Size: 131; Max: 285
seq_documentation_block:
ID AAGGAGG standard; RNA; 2141 bp.
XX
AC AAGGAGG285;
XX
DT 29-JAN-1991 (first entry)
XX
DE Human Tumour Necrosis Factor Receptor (DNA insert).
XX
KW Tumour necrosis factor binding protein; TNF R1; TNF-receptor;
lambdaTNF-R2; rTNF-R8; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..177
FT /tag a
FT /label huTNF-R
XX
PN KP393438-A.
XX
PD 24-OCT-1990.
XX
XX 06 APR 1990. YCEP 6156624.
XX
XX 21-JUN-1989. B95B 2926292.
XX 21-APR-1989. B95B-8914161.
XX
XX (BOU ) BOEHRINGER INGELHEIMINT.
XX
PI Hauptmann R, Himmeler A, Maurer-Fody L, Stratowa O.
XX
XX WPI; 1990 321987/43.
XX
XX P-PSDB; AAR07451.
XX
XX cDNA encoding TNF binding protein and TNF receptor fused in
XX tumour treatment used to understand mechanism to TNF action
XX
XX Disclosure: Fig 91(1-2); 51pp; German.
XX
XX rTNF-R8 (AAGGAGG284) was used to screen the HSv1.1 cDNA library.
XX lambdaTNF-R2 encodes the rTNF-R2 and was used to

```


[illegible]

```
seq_name: 271527_10_1014_1_100seq[1000000] AA006284
seq_documentation_block:
ID AA006284 standard; DNA; 2178 BP.
XX
XX AC AA006284;
XX
XX 29-JAN-1997 (first entry)
```

```

84  ysGluSerGlySerPheThrAlaSerGluAsnHisLeuAraHisCysLeu 100
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
495  CTCATAAAGCCACCTTACAGCTTCCAGAACACAGCTCAGACAGTCTCTC 544
101  SerCysSerLysCysAraGlySerMetGlyGlnValGluIleSerSerCys 117
      ::::::::::::::::::::::::::::::::::::::::::::::::::
545  AATTGCATACATCTGTGGAAACAAATTTCTCAAGTGGAAATTTCTCTTG 594
117  sThrValAspArgAspPheValCysGlyCysArgGlySerAsnGlnIleArgH 134
      ::::::::::::::::::::::::::::::::::::::::::::::::::
595  CAAAGCTGACATCGCATACGGTCTGTGGGTCGCAAGAGAACCAATTCACGC 644
134  iSTyTrpSerGluAsnLeuPheGlnPheProAsnCysSerLeuCysLeu 150
      ::::::::::::::::::::::::::::::::::::::::::::::::::
645  OCTACCTGACGACAGCCGATTTCCACTGCTGCGACTGCGACGCCCTTCCTC 694
151  AsnGlyThrValHisLeuSerCysGlnIleuLysGlnAsnThrValCysTh 167
      ::::::::::::::::::::::::::::::::::::::::::::::::::
695  AATGCAATGCTGCAATATGCTGTGAAGAGAGAACAGACAGGTGTGTAA 744
167  rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
      ::::::::::::::::::::::::::::::::::::::::::::::::::
745  GUGCCACGACAGATCTCTCTAAGCGGAAATGAGTGGACACCCCTTCCAGCC 794
184  snCysLysSerLeuLysCysThrLysLeuCysLeuProGlnIleGlu 200
      ::::::::::::::::::::::::::::::::::::::::::::::::::
795  ACTGCCAAGAAAAATCAGGAATCTATCAAGCTGTGCTACCTCCAGTTCCA 844
201  AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuSerProLeuVa 217
      ::::::::::::::::::::::::::::::::::::::::::::::::::
845  AATGTCATAAACCGCCAGCATCTCAATCTGCGGTGCTGTGCGCTGTGCT 894
217  tLeuPheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetT 234
      ::::::::::::::::::::::::::::::::::::::::::::::::::
895  TATCTTCTTACGCTCTGCTCTTTATCTTATCTTATCTTACGCACTCAGCT 944
234  yAraTyroGlnArgTrpLysSerLysLeuTyrserIleValCysGlyLys 250
      ::::::::::::::::::::::::::::::::::::::::::::::::::
945  GTCGATATGCCAGCTGAGGAGGTCAGGCTGCTGCTGCTGCTGCTGCTGCT 994
251  SerThrProGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 267
      ::::::::::::::::::::::::::::::::::::::::::::::::::
995  TCAGTCTCTGTCAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAG 1044
267  uAlaProAsn.....ProSerPheSerProThrProGlyPheThrProT 282
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1045  AACTCCAGGCTCTATCCGAGGCTTCAGGCGCAACCCGCGCTTCAACCCCA 1094
282  hrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThr 298
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1095  CACTGAGCTTACGACACACCGCCAGCTTACGTCACGCTGCTGCTGCTGCT 1144
299  .....tyrThrProGlyAspCysProAsnPheAlaAlaTrp 310
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1145  CCATCAGAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
310  oArgArgGluValAlaProProTyroGlnGlyAlaAspProIleLeuAla 327
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1195  TCTAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
327  hrAlaLeuAlaSerAspProIleProAsnProLeuGlnGlySerTrpGluAsp 343
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1242  GATGCTCAATCCCTGTCGCAATCCCGGCGGCTGCTGCTGCTGCTGCTGCT 1291
344  ...SerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrIle 359
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1292  GTGCTGGGAGGCCAGCACAGAGGCTGACACTGACAGAGCTGCTGCTGCT 1341
359  glyrAlaValValGluAsnValProProLeuArgTrpLysGluPheValA 376
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1342  GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1391
376  rArgLeuGlyLeuSerAspHisGluIleAspArgLeuGluLeuGlnAsn 392

```

```

11  ::::::::::::::::::::::::::::::::::::::::::::::::::
1392  GGTCTCTGGGGCTGAGCGAGCAAGATGAGGCGGTGGAGAGCTGCACAAC 1441
393  GlyArgCysLeuArgGluAlaGlnTyTrpSerMetLeuAlaThrTrpArgAr 409
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1442  GGGNTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1491
409  gAcqThrProArgArgGluAlaThrLeuGluLeuLeuGlyArgValLeuA 426
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1492  CCGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
426  rqAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAlaLeuCys 442
      ::::::::::::::::::::::::::::::::::::::::::::::::::
1542  GGTACATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1591
443  GlyProAla 445
      ::::::::::
1592  AGGCTGCTGCT 1600

```


